

# Untitled

Title: US- 10- 574- 297- 34  
 Perfect score: 5178  
 Sequence: 1 MYLDRFRQCPSSLQI PRSAW . . . . . AAGDRI NI PWSFHAGYRYSF 1010  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 3405708 seqs, 601879884 residues  
 Total number of hits satisfying chosen parameters: 3405708  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post - processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

## RESULT 2

ABU22871

ID ABU22871 standard; protein; 998 AA.

XX

AC ABU22871;

XX

DT 19- JUN- 2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #8398.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Bordetella pertussis.

XX

PN WO200277183- A2.

XX

PD 03- OCT- 2002.

XX

PF 21- MAR- 2002; 2002WO- US009107.

XX

PR 21- MAR- 2001; 2001US- 00815242.

PR

06- SEP- 2001; 2001US- 00948993.

PR

25- OCT- 2001; 2001US- 0342923P.

PR

08- FEB- 2002; 2002US- 00072851.

PR

06- MAR- 2002; 2002US- 0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW

PI

Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003- 029926/ 02.

DR

N- PSDB; ACA26741.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 50795; 1766pp; English.

XX

OC The invention relates to an isolated nucleic acid comprising any one of  
 OC the 6213 antisense sequences given in the specification where expression  
 OC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 Page 1

# Untitled

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

XX  
SQ Sequence 998 AA;

Query Match 98.7% Score 5109; DB 6; Length 998;  
Best Local Similarity 99.9% Pred. No. 3.3e-295;  
Matches 997; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	13	LQI PRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQEGFDHRDNTLI	72
Db	1	MQI PRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQEGFDHRDNTLI	60
Qy	73	AVFDDGVGI NLDDDPDELGETAPPTLKDI HI SVEHKNPMSKPAI GVRVSGAGRALTLAGS	132
Db	61	AVFDDGVGI NLDDDPDELGETAPPTLKDI HI SVEHKNPMSKPAI GVRVSGAGRALTLAGS	120
Qy	133	TI DATEGGI PAVVRRGGTLELDGVTVAGGEGMEPMIVSDAGSRLSVRGGVLGGEAPGVGL	192
Db	121	TI DATEGGI PAVVRRGGTLELDGVTVAGGEGMEPMIVSDAGSRLSVRGGVLGGEAPGVGL	180
Qy	193	VRAAQGGQASI I DATLQSI LGPALI ADGGS I SVAGGS I DMDMGPFPPPPPLPGAPLAA	252
Db	181	VRAAQGGQASI I DATLQSI LGPALI ADGGS I SVAGGS I DMDMGPFPPPPPLPGAPLAA	240
Qy	253	HPPLDRVA AVHAGQDGKVT LREVALRAHG PQATGVYAYMPGSEI TLQGGTVSVQGGDDGAG	312
Db	241	HPPLDRVA AVHAGQDGKVT LREVALRAHG PQATGVYAYMPGSEI TLQGGTVSVQGGDDGAG	300
Qy	313	VWAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVWNTVLR T AKSLAAGV	372
Db	301	VWAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVWNTVLR T AKSLAAGV	360
Qy	373	SAQHGGRVTLRQTRI ETAGAGAEGL SVLGFEPQSGSGPASVDMQGGSI TTTGNRAAGI AL	432
Db	361	SAQHGGRVTLRQTRI ETAGAGAEGL SVLGFEPQSGSGPASVDMQGGSI TTTGNRAAGI AL	420

Untitled

Qy	433	THGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAI SVTDTPLKLMPGALAS	492
Db	421	THGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAI SVTDTPLKLMPGALAS	480
Qy	493	STVSVRLTDGATAQGGNGVFLQQHSTI PVAVALESGALARGDI VADGNKPLDAGI SLSVA	552
Db	481	STVSVRLTDGATAQGGNGVFLQQHSTI PVAVALESGALARGDI VADGNKPLDAGI SLSVA	540
Qy	553	SGAAWHGATQVLQSATLGKGGTWVNADSRVQDMSMRGGRVEFQAPAPEASYKTLTLQTL	612
Db	541	SGAAWHGATQVLQSATLGKGGTWVNADSRVQDMSMRGGRVEFQAPAPEASYKTLTLQTL	600
Qy	613	DGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTCGGQGNAT	672
Db	601	DGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTCGGQGNAT	660
Qy	673	FRLANVGKAVDLGTWRYSLAEDPKTHWVSLQFAGQALSGAANAAVNAADLSSI ALAESNA	732
Db	661	FRLANVGKAVDLGTWRYSLAEDPKTHWVSLQFAGQALSGAANAAVNAADLSSI ALAESNA	720
Qy	733	LDKRLGELRLRADAGGPWARTFSEKQI SNRHARAYDQTVSGLEI GLDRGWSASGGFWYA	792
Db	721	LDKRLGELRLRADAGGPWARTFSEKQI SNRHARAYDQTVSGLEI GLDRGWSASGGFWYA	780
Qy	793	GGLLGITYADRTYPGDGGGKVKGLHVGGYAAVVDGGYYLDTVLRLGRYDQQYNI AGTDG	852
Db	781	GGLLGITYADRTYPGDGGGKVKGLHVGGYAAVVDGGYYLDTVLRLGRYDQQYNI AGTDG	840
Qy	853	GRVTADYRTSGAAVSLGGRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANT	912
Db	841	GRVTADYRTSGAAVSLGGRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANT	900
Qy	913	ATLGRLGLRFGRRI ALAGGNI VQPYARLGMTQEFKSTGDVRTNGI GHAGAGRHGRVELGA	972
Db	901	ATLGRLGLRFGRRI ALAGGNI VQPYARLGMTQEFKSTGDVRTNGI GHAGAGRHGRVELGA	960
Qy	973	GVDAALGKGHNLASYEYAAGDRI NI PWSFHAGYRYSF	1010
Db	961	GVDAALGKGHNLASYEYAAGDRI NI PWSFHAGYRYSF	998